

FIGURE 1

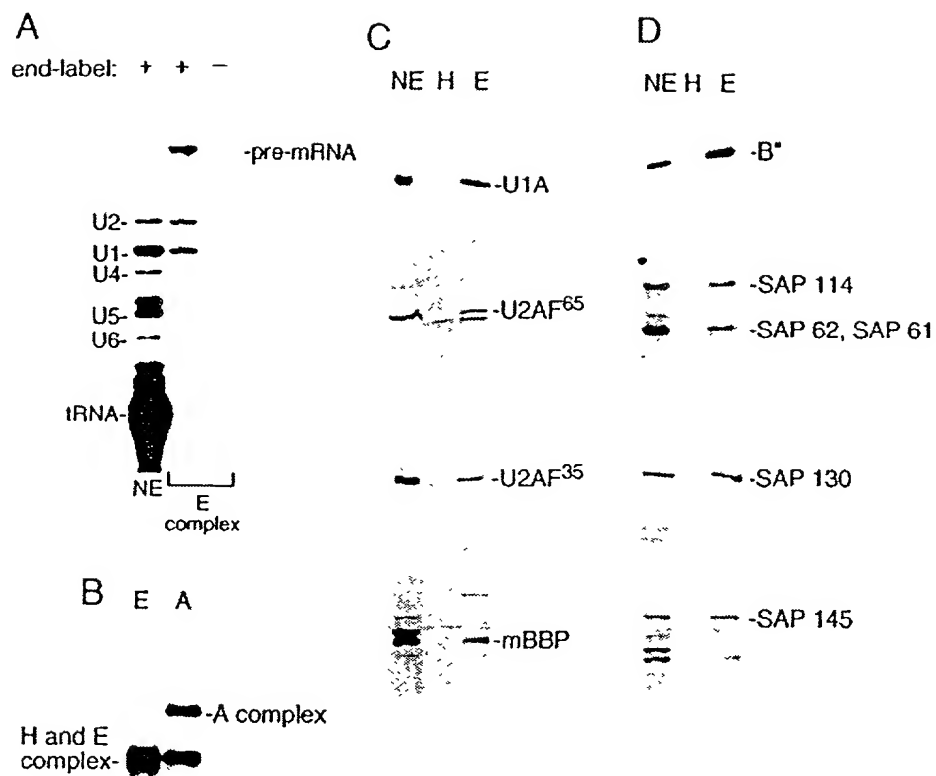


FIGURE 2

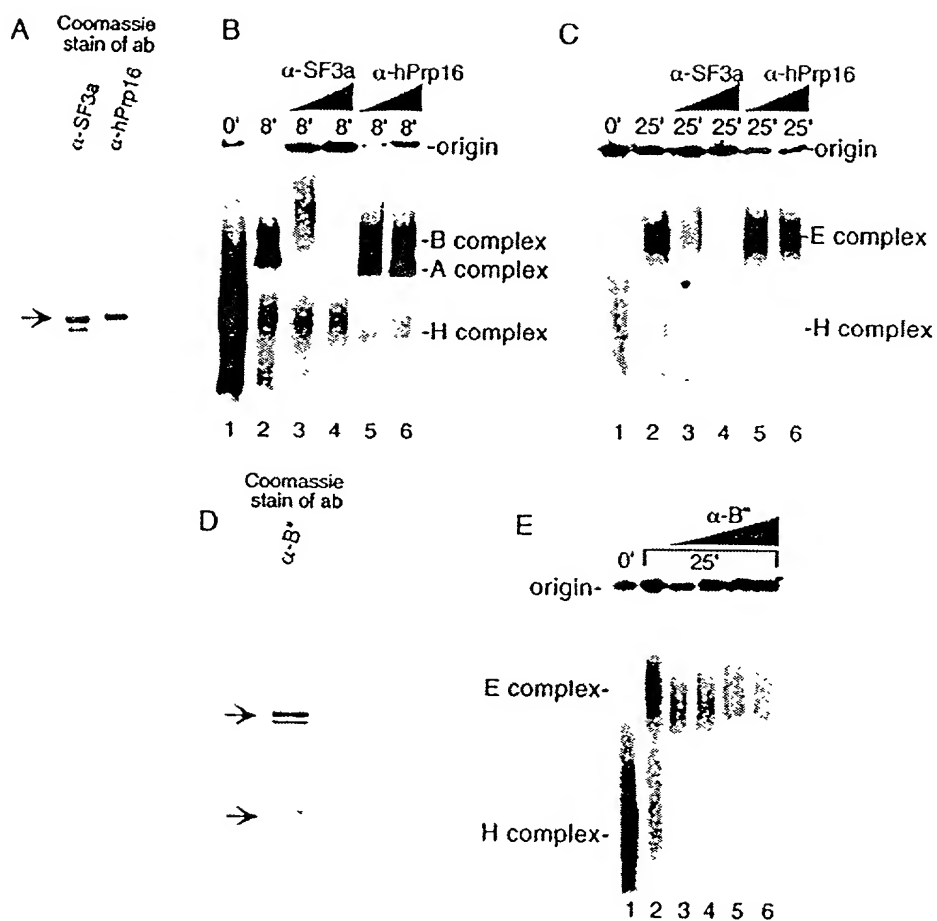


FIGURE 3

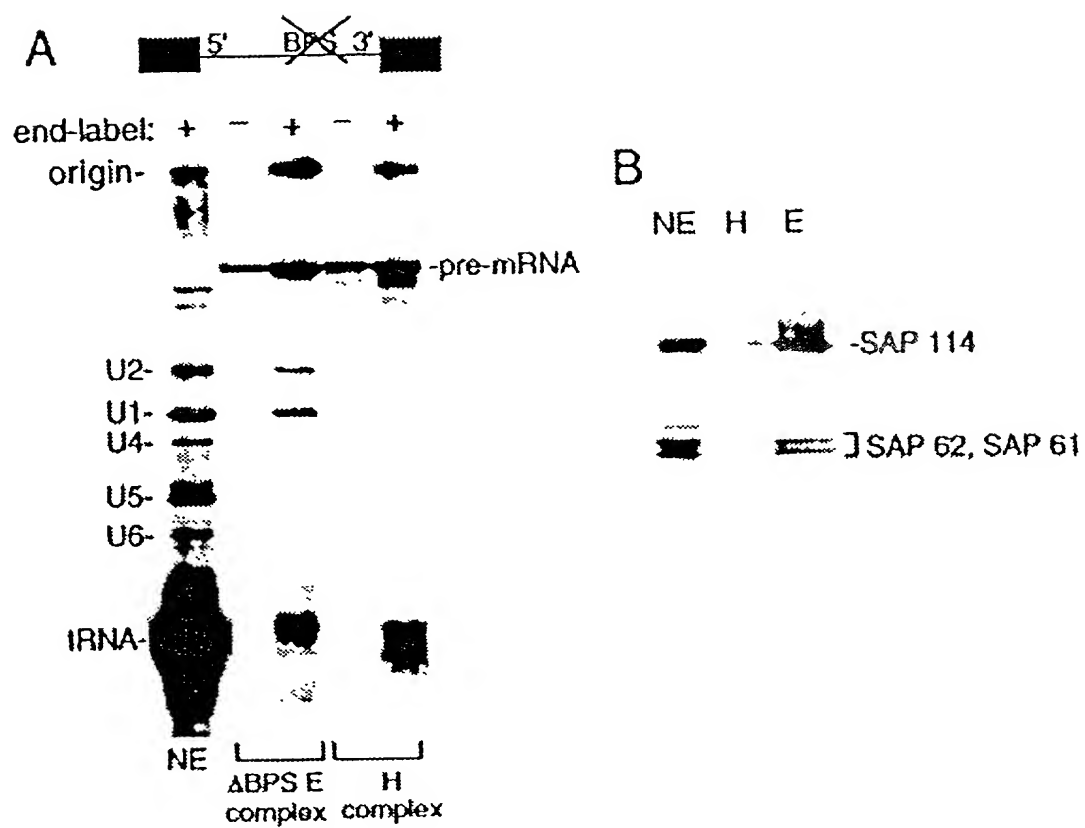


FIGURE 4

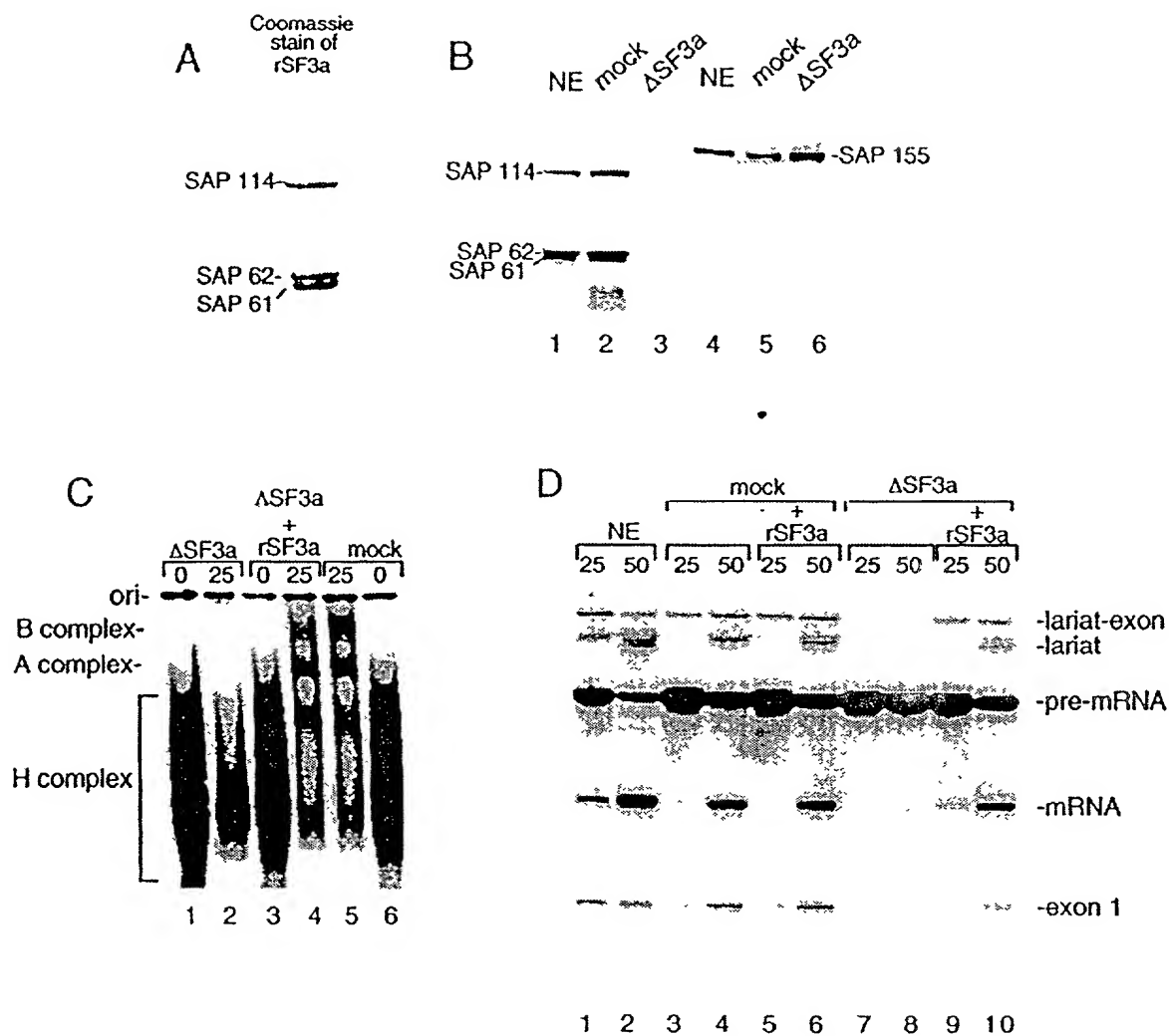


FIGURE 5

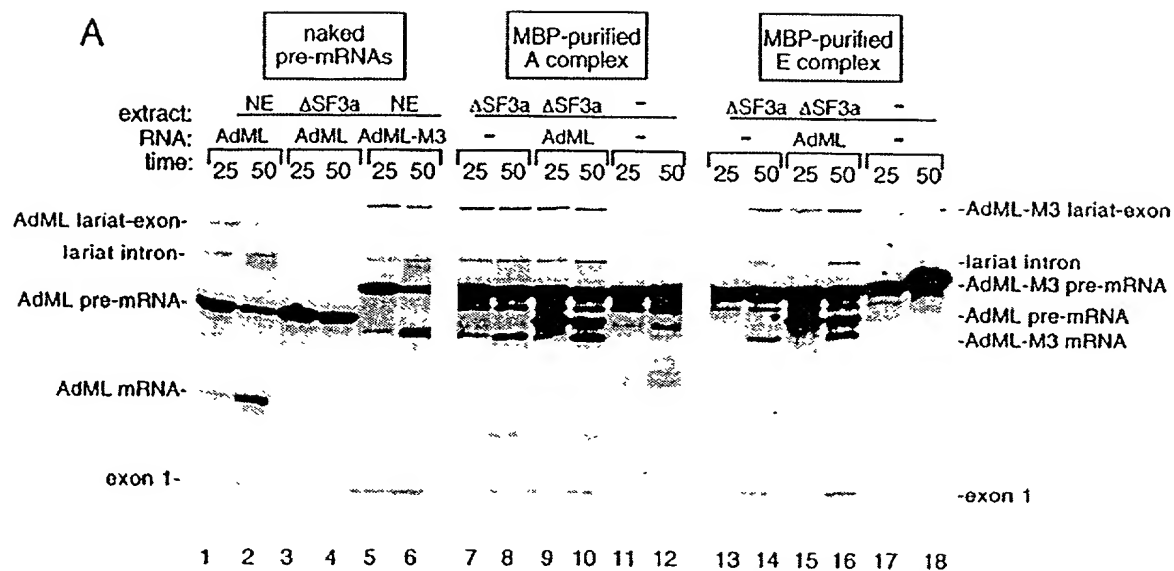


FIGURE 6

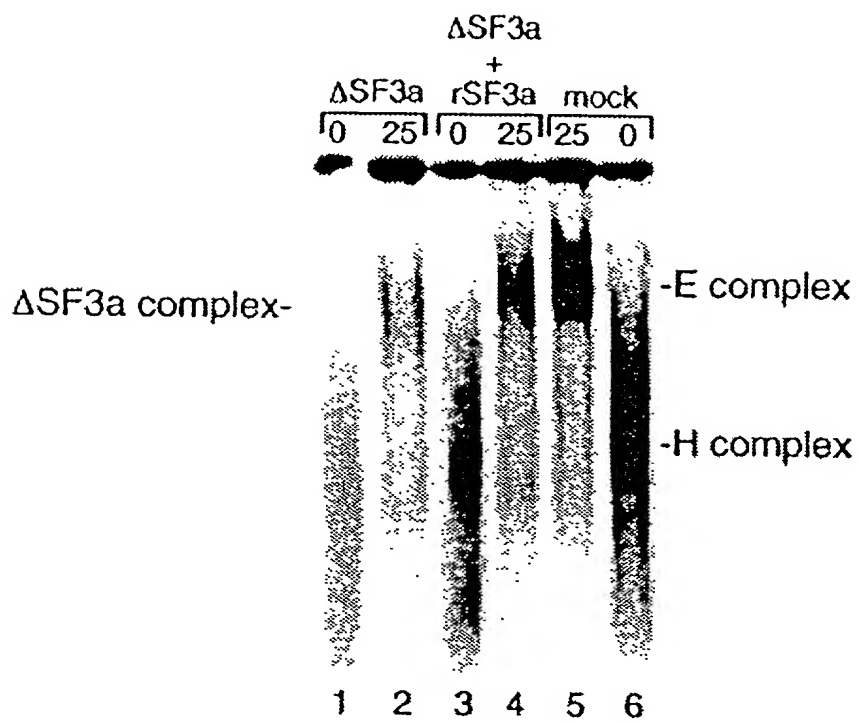


FIGURE 7

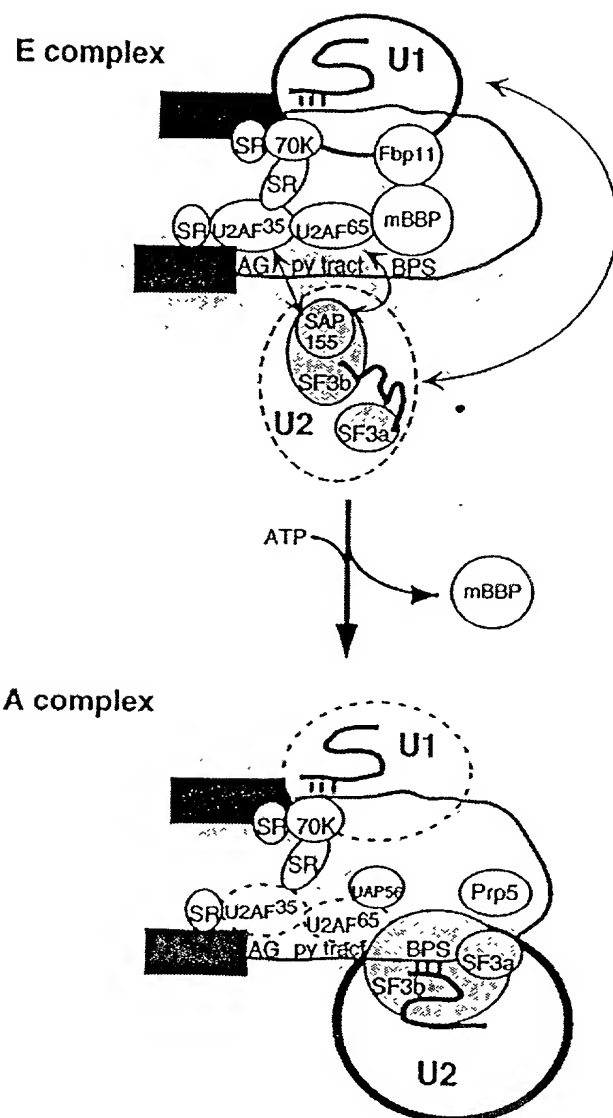


Figure 8

atg gct tct aac ttt act cag ttc gtt ctc gtc gac aat ggc gga act	48
Met Ala Ser Asn Phe Thr Gln Phe Val Leu Val Asp Asn Gly Gly Thr	
1 5 10 15	
ggc gac gtg act gtc gcc cca agc aac ttc gct aac ggg gtc gct gaa	96
Gly Asp Val Thr Val Ala Pro Ser Asn Phe Ala Asn Gly Val Ala Glu	
20 25 30	
tgg atc agc tct aac tcg cgt tca cag gct tac aaa gta acc tgt agc	144
Trp Ile Ser Ser Asn Ser Arg Ser Gln Ala Tyr Lys Val Thr Cys Ser	
35 40 45	
gtt cgt cag agc tct gcg cag aat cgc aaa tac acc atc aaa gtc gag	192
Val Arg Gln Ser Ser Ala Gln Asn Arg Lys Tyr Thr Ile Lys Val Glu	
50 55 60	
gtg cct aaa gtg gca acc cag act gtt ggt ggt gta gag ctt cct gta	240
Val Pro Lys Val Ala Thr Gln Thr Val Gly Gly Val Glu Leu Pro Val	
65 70 75 80	
gcc gca tgg cgt tcg tac tta aat atg gaa cta acc att cca att ttc	288
Ala Ala Trp Arg Ser Tyr Leu Asn Met Glu Leu Thr Ile Pro Ile Phe	
85 90 95	
gct acg aat tcc gac tgc gag ctt att gtt aag gca atg caa ggt ctc	336
Ala Thr Asn Ser Asp Cys Glu Leu Ile Val Lys Ala Met Gln Gly Leu	
100 105 110	
cta aaa gat gga aac ccg att ccc tca gca atc gca gca aac tcc ggc	384
Leu Lys Asp Gly Asn Pro Ile Pro Ser Ala Ile Ala Ala Asn Ser Gly	
115 120 125	
atc tac taa (SEQ ID NO: 1)	393
Ile Tyr (SEQ ID NO: 2)	
130	

Sequence alignment of the protein sequences shown in Figure 8. The sequences are aligned based on their amino acid composition, showing high similarity between the sequences. The alignment is shown in the figure, with the sequences numbered 1 through 130. The sequences are aligned in a way that shows the conserved regions and the variable regions. The alignment is shown in the figure, with the sequences numbered 1 through 130.

Figure 9

```

11881 tacgttttcgg ttttgtaggc cggacaaggc gttcacgccg catccggcat ttcacagcat
11941 tacttggtga tacgagtctg cgcgtcttcc agggcttcat cgacagtctg acgaccgctg
12001 gcggcggtga tcaccgcagt acgcacggca taccagaaag cggacatctg cgggatgttc
12061 ggcattgattt cacccttctg ggcgttttcc atggtggcgg caatacgtgg atctttcgcc
12121 aactcttcct cgtaagactt cagcgctacg gcaccagcg gtttgtcttt attaaccgct
12181 tccagacctt catcagtcag cagatagttt tccaggaact ctttcgccag ctctttgttc
12241 ggactggcgg cgtaataacc tgcgctcagc acgccaacga acggtttgga tgggtgacct
12301 ttgaaggctg gcagtaccgt tacaccataa ttcactttgc tgggtgcgat gttggacct
12361 gccacggggc cgttgatggt catcgctgtt tgcctttat taaaggcagc ttctgcgatg
12421 gagtaatcgg tgtctgcatt catgtgtttg tttttaatca ggtcaaccag gaaggtcaga
12481 cccgctttcg cgccagcgtt atccacgccc acgtctttaa tgcgtactt gccgttttca
12541 tacttgaacg cataaccccc gtcagcagca atcagcggcc aggtgaagta cggttcttgc
12601 aggttgaaca tcagcgcgct cttaccttcc gctttcagtt ctttatccag cgccgggatc
12661 tcttcccagg tttttggcgg gttcggcagc agatctttgt tataaatcag cgataacgct
12721 tcaacagcga tcgggtaagc aatcagcttg ccgttgtaac gtacggcatc ccaggtaaac
12781 ggatacagct tgccttgaa cgctttgtcc ggggtgattt cagccaacag gccagattga
12841 gcgtagccac caaagcggtc gtgtgccag aagataatgt cagggccatc gccagttgcc
12901 gcaacctgtg ggaatttctc ttccagtta tccgatgct caacgggtgac ttttaattccg
12961 gtatctttct cgaatttctt accgacttca gcgagaccgt tatagccttt atcgccgta
13021 atccagatta ccagtttacc ttcttcgatt ttggcgagag ccgagggcga aaacatcatc
13081 gtcgttaatg cggataatgc gaggatgcgt gcacctgtt ttattttcat aatctatgg
13141 ccttgttggt gaagtgtcgt tgaaaacacc taaacggact ctagtttctt tatacggcaa
13201 cctctttcca tctccttgc ccctacgccc caccgtcgtt ttgtgtgatc tctgttacg

```

SEQ ID NO: 3

MKIKTGARILALSALT'TMMFSASALAKIEEGKLVIWINGDKGYNGLAEVGGKFEKDTGIKVTVEHPDKLE
EKFPQVAATGDGPDIIFWAHDRFGGYAQSGLLAEITPDKAFQDKLYPFTWDAVRYNGKLIAYPIAVEALS
LIYNKDLLPNPPKTWEEIPALDKELKAKGKSALMFNLQEPYFTWPLIAADGGYAFKYENGKYDIKDVGV
NAGAKAGLTFLVDLIKNKHMNADTDYSIAEAAFNKGETAMTINGPWAWSNIDTSKVNYGVTVLPTFKGQP
SKPFVGVLSAGINAASPNKELAKEFLNYLLTDEGLEAVNKDKPLGAVALKSYYYEELAKDPRIAATMENA
QKGEIMPNIPQMSAFWYAVRTAVINAASGRQTVDEALKDAQTRITK (SEQ ID NO: 4)

CCCTCTTCCA